

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/805,694A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering            The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4      Non-ASCII            The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"                 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7      Skipped Sequences  
    (OLD RULES)         Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                           (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                           (i)       SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                           (xi)      SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                           This sequence is intentionally skipped  
  
                           Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)         Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                           <210> sequence id number  
                           <400> sequence id number  
                           000
  
- 9 ✓      Use of n's or Xaa's  
    (NEW RULES)         Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                           Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                           In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>  
    Response             Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220>       Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                           Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                           (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug"                 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PAGE: 1

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/09/805,694A**

DATE: 08/03/2001  
 TIME: 17:16:14

Input Set: I805694A.RAW

**This Raw Listing contains the General Information  
 Section and up to first 5 pages.**

1 <110> APPLICANT: Kinney, Anthony  
 2 <120> TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans  
 3 <130> FILE REFERENCE: BB1432 US NA  
 4 <140> CURRENT APPLICATION NUMBER: US/09/805,694A  
 5 <141> CURRENT FILING DATE: 2001-03-14  
 6 <150> EARLIER APPLICATION NUMBER: 60/189,823  
 7 <151> EARLIER FILING DATE: 2000-03-16  
 8 <160> NUMBER OF SEQ ID NOS: 16  
 9 <170> SOFTWARE: Microsoft Office 97  
 10 <210> SEQ ID NO 1  
 11 <211> LENGTH: 1156  
 12 <212> TYPE: DNA  
 13 <213> ORGANISM: chimeric construct  
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 16 ccagcatatc aactcatcgt tccatattgg accttgacct aaccaagttt accacacaga 120  
 17 aacagggtgtc ttactgttc caactatgga agagttagca tggacgtgtc taccataacc 180  
 18 acgaagaaga ggcaaagaga cttgagattt tcaagaataa ctcgaactat atcagggaca 240  
 19 tgaatgcaaa cagaaaatca ccccatcttc atcgtttagg attgaacaag tttgctgaca 300  
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 21 tcaaaatggc caacaagaaa atgaagaagg aacaatatc ttgtgacct ccacctgcat 420  
 22 catgggattg gaggaaaaaa ggtgtcatca cccaagtaaa gtaccaaggg ggctgtggaa 480  
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 32 acacgggtaa tttattagga gtgtgtggga tgaattattt cgcttcatac ccaaccaaag 1080  
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 42 actgactagt ctcttgatc ataagaaaaa gccaaaggaac aaaagaagac aaaacacaat 180  
 43 gagagtatcc tttgcatagc aatgtctaag ttcataaaat tcaaacaaaa acgcaatcac 240  
 44 acacagtgga catcacttat ccactagctg aatcaggatc gccgcgtcaa gaaaaaaaaa 300

Does Not Comply  
 Corrected Diskette Needed

See page 5

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/805,694A

DATE: 08/03/2001  
TIME: 17:16:14

Input Set: I805694A.RAW

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91      <211> LENGTH: 1600
92      <212> TYPE: DNA
93      <213> ORGANISM: Glycine max
94      <400> SEQUENCE: 3

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/805,694A

DATE: 08/03/2001  
TIME: 17:16:14

Input Set: I805694A.RAW

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111 cgggatccat gttggcacct catgtgaatc caatatcaga tgagtatacc atagtgtctga 1020
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123 <211> LENGTH: 454
124 <212> TYPE: PRT
125 <213> ORGANISM: Glycine max
126 <400> SEQUENCE: 4
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128 1 5 10 15
129 Leu Phe Leu Met Ser Asn Ser Thr Arg Val Phe Lys Thr Asp Ala Gly
130 20 25 30
131 Glu Met Arg Val Leu Lys Ser His Gly Gly Arg Ile Phe Tyr Arg His
132 35 40 45
133 Met His Ile Gly Phe Ile Ser Met Glu Pro Lys Ser Leu Phe Val Pro
134 50 55 60
135 Gln Tyr Leu Asp Ser Asn Leu Ile Ile Phe Ile Arg Arg Gly Glu Ala
136 65 70 75 80
137 Lys Leu Gly Phe Ile Tyr Asp Asp Glu Leu Ala Glu Arg Arg Leu Lys
138 85 90 95
139 Thr Gly Asp Leu Tyr Met Ile Pro Ser Gly Ser Ala Phe Tyr Leu Val
140 100 105 110
141 Asn Ile Gly Glu Gly Gln Arg Leu His Val Ile Cys Ser Ile Asp Pro
142 115 120 125
143 Ser Thr Ser Leu Gly Leu Glu Thr Phe Gln Ser Phe Tyr Ile Gly Gly
144 130 135 140

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# RAW SEQUENCE LISTING

## PATENT APPLICATION US/09/805,694A

 DATE: 08/03/2001  
 TIME: 17:16:14

Input Set: I805694A.RAW

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145      Gly Ala Asn Ser His Ser Val Leu Ser Gly Phe Glu Pro Ala Ile Leu
146      145                      150                      155                      160
147      Glu Thr Ala Phe Asn Glu Ser Arg Thr Val Val Glu Glu Ile Phe Ser
148                      165                      170                      175
149      Lys Glu Leu Asp Gly Pro Ile Met Phe Val Asp Asp Ser His Ala Pro
150                      180                      185                      190
151      Ser Leu Trp Thr Lys Phe Leu Gln Leu Lys Lys Asp Asp Lys Glu Gln
152                      195                      200                      205
153      Gln Leu Lys Lys Met Met Gln Asp Gln Glu Glu Asp Glu Glu Glu Lys
154                      210                      215                      220
155      Gln Thr Ser Arg Ser Trp Arg Lys Leu Leu Glu Thr Val Phe Gly Lys
156      225                      230                      235                      240
157      Val Asn Glu Lys Ile Glu Asn Lys Asp Thr Ala Gly Ser Pro Ala Ser
158                      245                      250                      255
159      Tyr Asn Leu Tyr Asp Asp Lys Lys Ala Asp Phe Lys Asn Ala Tyr Gly
160                      260                      265                      270
161      Trp Ser Lys Ala Leu His Gly Gly Glu Tyr Pro Pro Leu Ser Glu Pro
162                      275                      280                      285
163      Asp Ile Gly Val Leu Leu Val Lys Leu Ser Ala Gly Ser Met Leu Ala
164                      290                      295                      300
165      Pro His Val Asn Pro Ile Ser Asp Glu Tyr Thr Ile Val Leu Ser Gly
166      305                      310                      315                      320
167      Tyr Gly Glu Leu His Ile Gly Tyr Pro Asn Gly Ser Lys Ala Met Lys
168                      325                      330                      335
169      Thr Lys Ile Lys Gln Gly Asp Val Phe Val Val Pro Arg Tyr Phe Pro
170                      340                      345                      350
171      Phe Cys Gln Val Ala Ser Arg Asp Gly Pro Leu Glu Phe Phe Gly Phe
172                      355                      360                      365
173      Ser Thr Ser Ala Arg Lys Asn Lys Pro Gln Phe Leu Ala Gly Ala Ala
174                      370                      375                      380
175      Ser Leu Leu Arg Thr Leu Met Gly Pro Glu Leu Ser Ala Ala Phe Gly
176      385                      390                      395                      400
177      Val Ser Glu Asp Thr Leu Arg Arg Ala Val Asp Ala Gln His Glu Ala
178                      405                      410                      415
179      Val Ile Leu Pro Ser Ala Trp Ala Ala Pro Pro Glu Asn Ala Gly Lys
180                      420                      425                      430
181      Leu Lys Met Glu Glu Glu Pro Asn Ala Ile Arg Ser Phe Ala Asn Asp
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183      Val Val Met Asp Val Phe
184                      450

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185      <210> SEQ ID NO 5
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188      <213> ORGANISM: Glycine max
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190      <221> NAME/KEY: unsure
191      <222> LOCATION: (9)
192      <223> OTHER INFORMATION: n = A, C, G, or T
193      <220> FEATURE:
194      <221> NAME/KEY: unsure

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/805,694A

DATE: 08/03/2001  
TIME: 17:16:14

Input Set: I805694A.RAW

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 197 <220> FEATURE:  
 198 <221> NAME/KEY: unsure  
 199 <222> LOCATION: (392)..(393)  
 200 <223> OTHER INFORMATION: n = A, C, G, or T  
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 206 <221> NAME/KEY: unsure  
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 211 <222> LOCATION: (478)  
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 224 <211> LENGTH: 75  
 225 <212> TYPE: PRT  
 226 <213> ORGANISM: Glycine max  
 227 <400> SEQUENCE: 6  
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 230 Phe Val Ala Gln Glu Val Val Val Gln Thr Glu Ala Lys Thr Cys Glu  
 231 20 25 30  
 232 Asn Leu Ala Asp Thr Tyr Arg Gly Pro Cys Phe Thr Thr Gly Ser Cys  
 233 35 40 45  
 234 Asp Asp His Cys Lys Asn Lys Glu His Leu Leu Arg Gly Arg Cys Arg  
 235 50 55 60  
 236 Asp Asp Phe Arg Cys Trp Cys Thr Lys Asn Cys  
 237 65 70 75  
 238 <210> SEQ ID NO 7  
 239 <211> LENGTH: 30  
 240 <212> TYPE: DNA  
 241 <213> ORGANISM: Artificial Sequence  
 242 <220> FEATURE:  
 243 <223> OTHER INFORMATION: Description of Artificial Sequence: P34 gene primer  
 244 <400> SEQUENCE: 7

Location and description  
of unknowns (n's) is  
mandatory.

463 463  
Errored

Input Set: I805694A.RAW

| Line | ? Error/Warning                       | Original Text                             |
|------|---------------------------------------|---|
| 214  | W "N" or "Xaa" used: Feature required | acacagctng cacatattac atacacgtga atcactaa |
| 220  | W "N" or "Xaa" used: Feature required | tgggcgctgc atcaatgacc ctatgtanta tnntatat |
| 221  | W "N" or "Xaa" used: Feature required | atagatgcat gtactgtgca taacggctga gttatgtc |